Gerald Amiel Ballena

♦ Metro Manila, Philippines

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Experience

Project Technical Specialist (Contract)

University of the Philippines, College of Public Health

2024 - Present

- Designed and implemented dynamic metagenomics pipelines enabling accurate profiling of microbial communities.
- Automated data preprocessing workflows using Snakemake, reducing manual load by 90% when data is available while also enhancing reproducibility.
- Collaborated with multidisciplinary teams to ensure robust data analysis and visualization tailored for research publications.

Ongoing Key Projects

- Bioinformatics Workflow Development: Designed modular pipelines for omics data analysis with a focus on quality control and scalable workflows.
- Shannon Entropy Analysis of K-mers: Quantified sequence complexity using entropy-based metrics for diversity assessment.
- **Pipeline Automation:** Developed tools for dependency management and alias creation to streamline workflows.

Certifications

Education

University of the Philippines Diliman

Graduated: July 2022

Thesis: In silico assessment of the association of pathogenicity and metal-resistance potential of Fusarium spp. . Preprint Link

Accomplishments: DOST ASTHRDP-Scholarship

University of the Philippines Baguio

Graduated: June 2018

Thesis: Bioelectrocatalysis by Novel Electrogenic Alkaliphilic Bacteria Bacillus sp. BAB-3442 Using

Skills

Programming

Python, R, Bash, Perl

Bioinformatics Tools

- Metagenomics: Kraken2, MetaPhlAn, HUMAnN
- Assembly & Binning: MEGAHIT, METAWRAP, CheckM
- Genomics: CLC Workbench, Roary, MinHash
- Quality Control: FastQC, BUSCO, QUAST
- Trimming: Trimmomatic, Sickle, Cutadapt
- Phylogenetics: RaxML, FastTree, IQ-TREE, phyML, BEAST
- Gene Ontology: KEGG, GOseq
- Annotation: Prokka, ShortBRED, EggNOG-mapper
- Others: DESeq2, BBMap Suite, anvio-8, SPAdes

Data Analysis & Visualization

- Machine Learning: scikit-learn, caret (R)
- Visualization: ggplot2, Plotly, Krona, Shiny, Seaborn, Tableau

Technical Skills

- Version Control: Git, GitHub
- High-Performance Computing: Slurm
- Workflow Automation: Snakemake, Conda, YAML
- Virtualization: Docker, WSL2

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Certifications

•	AI Fundamentals
•	Intermediate R
•	RNA-Seq with Bioconductor in R

References

Available only upon request and shortlisted.